



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 10/613228

TO: Nita M Minnfield
Location: REM/3C01/3C18
Art Unit: 1645
Monday, August 29, 2005

Case Serial Number: 10/613228

From: Mary Jane Ruhl
Location: Biotech-Chem Library
Remsen 1-A-62
Phone: 571-272-2524

maryjane.ruhl@uspto.gov

Search Notes

Examiner Minnfield,

Here are the results for your recent search request.

Please feel free to contact me if you have any questions about these results.

Thank you for using STIC services. We appreciate the opportunity to serve you.

Sincerely,

Mary Jane Ruhl
Technical Information Specialist
STIC
Remsen 1-A-62
Ext. 22524

*Reviewed
10/05
mru*



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From: Minnifield, Nita
Sent: Wednesday, August 24, 2005 12:37 PM
To: STIC-Biotech/ChemLib
Subject: interference sequence search request

10/613228

STIC

Please do an interference sequence search on SEQ ID NO: 1 of this application.

Please show first 30 results/alignments.

Please provide a paper copy of all results.

Thanks,
Minnifield,
71976
Art Unit 1645
Office REM-3C01
Mailbox REM-3C18
571-272-0860

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2-
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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Copyright (c) 1993 - 2005 Compugen Ltd.	GenCore version 5.1.6					
Run on:	August 28, 2005, 22:52:19 ; Search time 373 Seconds (without alignments)					
Scoring table:	IDENTITY_NUC Gapext 1.0					
Title:	US-10-613-228A-1					
Searched:	7331713 seqs, 3271544945 residues					
Total number of hits satisfying chosen parameters:	14663426					
Minimum DB seq length:	0					
Maximum DB seq length:	200000000					
Post-processing:	Minimum Match 0% Maximum Match 100% Listing first 90 summaries					
Database :	Published Applications NA.* /cgm2_6/ptodata/1/pubpna/PCRTS_PUBCOMB.seq.* 1: /cgm2_6/ptodata/1/pubpna/PCRN_NEW_PUB.seq.* 2: /cgm2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.* 3: /cgm2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.* 4: /cgm2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.* 5: /cgm2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.* 6: /cgm2_6/ptodata/1/pubpna/PCRTS_PUBCOMB.seq.* 7: /cgm2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.* 8: /cgm2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.* 9: /cgm2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.* 10: /cgm2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.* 11: /cgm2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.* 12: /cgm2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.* 13: /cgm2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.* 14: /cgm2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.* 15: /cgm2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.* 16: /cgm2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.* 17: /cgm2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.* 18: /cgm2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.* 19: /cgm2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq.* 20: /cgm2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq.* 21: /cgm2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.* 22: /cgm2_6/ptodata/1/pubpna/US10J_PUBCOMB.seq.* 23: /cgm2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.* 24: /cgm2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.* 25: /cgm2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.* 26: /cgm2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*					
Pred. No.	is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.					
Result No.	Query Match Length DB ID Description					
	%					
	Match Length DB ID					
	Score					
	Match Length DB ID					
	Description					
	Summary					
1	22	100.0	22	18	US-10-613-228A-1	Sequence 1, Appli
2	22	100.0	22	20	US-10-816-220-152	Sequence 152, App
3	22	100.0	22	21	US-10-644-052A-290	Sequence 290, App
4	20.4	92.7	618	20	US-10-363-345A-34257	Sequence 34257, A
5	20.4	92.7	618	20	US-10-363-345A-34258	Sequence 34258, A
6	20.4	92.7	618	21	US-10-363-483A-34257	Sequence 34257, A
7	20.4	92.7	618	21	US-10-363-483A-34258	Sequence 34258, A
8						Sequence 40287, A
9						Sequence 40288, A
10						Sequence 40289, A
11						Sequence 40290, A
12						Sequence 40291, A
13						Sequence 40292, A
14						Sequence 40293, A
15						Sequence 40294, A
16						Sequence 40295, A
17						Sequence 40296, A
18						Sequence 40297, A
19						Sequence 40298, A
20						Sequence 40299, A
21						Sequence 40300, A
22						Sequence 40301, A
23						Sequence 40302, A
24						Sequence 40303, A
25						Sequence 40304, A
26						Sequence 40305, A
27						Sequence 40306, A
28						Sequence 40307, A
29						Sequence 40308, A
30						Sequence 40309, A
31						Sequence 40310, A
32						Sequence 40311, A
33						Sequence 40312, A
34						Sequence 40313, A
35						Sequence 40314, A
36						Sequence 40315, A
37						Sequence 40316, A
38						Sequence 40317, A
39						Sequence 40318, A
40						Sequence 40319, A
41						Sequence 40320, A
42						Sequence 40321, A
43						Sequence 40322, A
44						Sequence 40323, A
45						Sequence 40324, A
46						Sequence 40325, A
47						Sequence 40326, A
48						Sequence 40327, A
49						Sequence 40328, A
50						Sequence 40329, A
51						Sequence 40330, A
52						Sequence 40331, A
53						Sequence 40332, A
54						Sequence 40333, A
55						Sequence 40334, A
56						Sequence 40335, A
57						Sequence 40336, A
58						Sequence 40337, A
59						Sequence 40338, A
60						Sequence 40339, A
61						Sequence 40340, A
62						Sequence 40341, A
63						Sequence 40342, A
64						Sequence 40343, A
65						Sequence 40344, A
66						Sequence 40345, A
67						Sequence 40346, A
68						Sequence 40347, A
69						Sequence 40348, A
70						Sequence 40349, A
71						Sequence 40350, A
72						Sequence 40351, A
73						Sequence 40352, A
74						Sequence 40353, A
75						Sequence 40354, A
76						Sequence 40355, A
77						Sequence 40356, A
78						Sequence 40357, A
79						Sequence 40358, A
80						Sequence 40359, A

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No. Score Query Match Length DB ID Description

%

Match Length DB ID

Score

Match Length DB ID

Description

Summary

8

20.4

92.7

619

20

US-10-363-345A-40287

Sequence 40287, A

9

20.4

92.7

619

20

US-10-363-345A-40288

Sequence 40288, A

10

20.4

92.7

619

21

US-10-363-483A-40288

Sequence 40288, A

11

20.4

92.7

619

21

US-10-363-483A-40289

Sequence 40289, A

12

20.4

92.7

761

20

US-10-363-345A-2025

Sequence 2025, AP

13

20.4

92.7

761

21

US-10-363-483A-2025

Sequence 2025, AP

14

20.4

92.7

761

21

US-10-363-483A-2026

Sequence 2026, AP

15

20.4

92.7

1024

20

US-10-363-345A-7204

Sequence 7204, AP

16

20.4

92.7

1024

21

US-10-363-483A-7203

Sequence 7203, AP

17

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

18

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

19

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

21

20.4

92.7

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21

US-10-363-483A-7204

Sequence 7204, AP

22

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

23

20.4

92.7

1024

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US-10-363-483A-7204

Sequence 7204, AP

24

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

25

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

26

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

27

20.4

92.7

1024

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US-10-363-483A-7204

Sequence 7204, AP

28

20.4

92.7

1024

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US-10-363-483A-7204

Sequence 7204, AP

29

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

30

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

31

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

32

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

33

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

34

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

35

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

36

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

37

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

38

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

39

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

40

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

41

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

42

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

43

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

44

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

45

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

46

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

47

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

48

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

49

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

50

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

51

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

52

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

53

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

54

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

55

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

56

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

57

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

58

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

59

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

60

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

61

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

62

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

63

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

64

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

65

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

66

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

67

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

68

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

69

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

70

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

71

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

72

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

73

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

74

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

75

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

76

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

77

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

78

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

79

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

80

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

81

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204, AP

82

20.4

92.7

1024

21

US-10-363-483A-7204

Sequence 7204,

RESULT 1
US-10-613-228a-1
; Publication No. US20040092472A1
; Sequence 1, Application US/10613228A
GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M
; TITLE OF INVENTION: NUCLEIC ACID COMPOSITIONS FOR STIMULATING IMMUNE RESPONSES
; FILE REFERENCE: C1037.70045US00
; CURRENT APPLICATION NUMBER: US/10/613_228A
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: US 60/394,193
; PRIOR FILING DATE: 2002-07-03
; NUMBER OF SEQ ID NOS: 3
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Oligodeoxynucleotide
US-10-613-228a-1

Query Match 100.0%; Score 22; DB 18; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 22; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

QY 1 TCGTCGTTTCTGGCGTTTT 22
Db 1 TCGTCGTTTCTGGCGTTTT 22

RESULT 2
US-10-816-220-152
; Sequence 152, Application US/0816220
; Publication No. US2004023570A1
GENERAL INFORMATION:
; APPLICANT: Davis, Heather L
; APPLICANT: McCluskie, Michael J
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID OIL-IN-WATER FORMULATIONS AND
FILE REFERENCE: C1037.70039US01
CURRENT APPLICATION NUMBER: US/10/816,220
CURRENT FILING DATE: 2004-04-01
PRIOR APPLICATION NUMBER: US 60/459,920
PRIOR FILING DATE: 2003-04-02
PRIOR APPLICATION NUMBER: US 60/461,903
PRIOR FILING DATE: 2003-04-10
NUMBER OF SEQ ID NOS: 434
SOFTWARE: PatentIn version 3.2
SEQ ID NO 152
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide
US-10-816-220-152

Query Match 100.0%; Score 22; DB 18; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 22; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

QY 1 TCGTCGTTTCTGGCGTTTT 22
Db 1 TCGTCGTTTCTGGCGTTTT 22

RESULT 3
US-10-644-052A-290
; Publication No. US20050059619A1
GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M
; APPLICANT: Samulowitz, Ulrike
; APPLICANT: Vollmer, Joerg
; APPLICANT: Uhlmann, Eugen
; APPLICANT: Jurk, Marion
; APPLICANT: Lipford, Grayson
; APPLICANT: Rankin, Robert
GENERAL INFORMATION:
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACIDS
; FILE REFERENCE: C1037.70045US00
; CURRENT APPLICATION NUMBER: US/10/644_052A
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: US 60/404,479
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/404,820
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/429,701
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: US 60/447,377
; PRIOR FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 290
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligodeoxynucleotide
US-10-644-052A-290

Query Match 100.0%; Score 22; DB 21; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 22; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

QY 1 TCGTCGTTTCTGGCGTTTT 22
Db 1 TCGTCGTTTCTGGCGTTTT 22

RESULT 4
US-10-363-345A-34257
; Sequence 34257, Application US/10363345A
; Publication No. US20040234960A1
GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
FILE REFERENCE: E011/1227
CURRENT APPLICATION NUMBER: US/10/363,345A
CURRENT FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 40712
SEQ ID NO 34257
LENGTH: 618
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
OTHER INFORMATION: CpG-island No: 34257
US-10-363-345A-34257

Query Match 100.0%; Score 22; DB 20; Length 22;

Query Match 92.7%; Score 20.4; DB 20; Length 618;
 Best Local Similarity 95.5%; Pred. No. 30;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTCTGGCGTTT 22
 Db 98 TCGTCGTTTCTGGCGTTT 119

RESULT 5
 US-10-363-345A-4258/C
 ; Sequence 34258, Application US/10363345A
 ; Publication No. US2004040234960A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alexander Olek
 ; APPLICANT: Christian Piepenbrock
 ; APPLICANT: Kurt Berlin
 ; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
 FILE REFERENCE: 82011
 CURRENT APPLICATION NUMBER: US/10/363, 483A
 CURRENT FILING DATE: 2003-03-03
 NUMBER OF SEQ ID NOS: 40712
 SEQ ID NO 34258
 LENGTH: 618
 TYPE: DNA
 FEATURE:
 ORGANISM: Artificial Sequence
 OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
 US-10-363-345A-34258

Query Match 92.7%; Score 20.4; DB 20; Length 618;
 Best Local Similarity 95.5%; Pred. No. 30;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTCTGGCGTTT 22
 Db 521 TCGTCGTTTCTGGCGTTT 500

RESULT 6
 US-10-363-483A-34257
 ; Sequence 34257, Application US/103633483A
 ; Publication No. US2005006401A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alexander Olek
 ; APPLICANT: Christian Piepenbrock
 ; APPLICANT: Kurt Berlin
 ; TITLE OF INVENTION: Method for determining the degree of methylation of defined
 FILE REFERENCE: E01/1227
 CURRENT APPLICATION NUMBER: US/10/363, 345A
 CURRENT FILING DATE: 2003-03-03
 NUMBER OF SEQ ID NOS: 40712
 SEQ ID NO 40287
 LENGTH: 619
 TYPE: DNA
 FEATURE:
 ORGANISM: Artificial Sequence
 OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
 US-10-363-345A-40287

Query Match 92.7%; Score 20.4; DB 20; Length 619;
 Best Local Similarity 95.5%; Pred. No. 30;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTCTGGCGTTT 22
 Db 190 TCGTCGTTTCTGGCGTTT 211

RESULT 7
 US-10-363-483A-34258/C
 ; Sequence 34258, Application US/10363345A
 ; Publication No. US2004040234960A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alexander Olek
 ; APPLICANT: Christian Piepenbrock
 ; APPLICANT: Kurt Berlin
 ; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
 FILE REFERENCE: 82011
 CURRENT APPLICATION NUMBER: US/10/363, 483A
 CURRENT FILING DATE: 2003-03-03
 NUMBER OF SEQ ID NOS: 40712
 SEQ ID NO 34258
 LENGTH: 618
 TYPE: DNA
 FEATURE:
 ORGANISM: Artificial Sequence
 OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
 US-10-363-483A-34258

Query Match 92.7%; Score 20.4; DB 21; Length 618;
 Best Local Similarity 95.5%; Pred. No. 30;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTCTGGCGTTT 22
 Db 98 TCGTCGTTTCTGGCGTTT 119

RESULT 9
 US-10-363-345A-40288/C
 ; Sequence 40288, Application US/10363345A
 ; Publication No. US2004040234960A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alexander Olek
 ; APPLICANT: Christian Piepenbrock
 ; APPLICANT: Kurt Berlin

; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363, 345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 40288
; LENGTH: 619
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: Cpg-island No: 40288
; US-10-363-345A-40288

Query Match 92.7%; Score 20.4; DB 20; Length 619;
Best Local Similarity 95.5%; Pred. No. 30; Mismatches 0; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGTGTGTTTCGTCGGTTT 22
Db 430 TCGTGTGTTTCGTCGGTTT 409

RESULT 10
US-10-363-483A-40287
Sequence 40287, Application US/10363483A
Publication No. US2005006401A1
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
FILE REFERENCE: 82011
CURRENT APPLICATION NUMBER: US/10/363, 483A
CURRENT FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 40712
SEQ ID NO 40287
LENGTH: 619
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
OTHER INFORMATION: Cpg-island No: 40287
US-10-363-483A-40287

Query Match 92.7%; Score 20.4; DB 20; Length 619;
Best Local Similarity 95.5%; Pred. No. 30; Mismatches 0; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGTGTGTTTCGTCGGTTT 22
Db 430 TCGTGTGTTTCGTCGGTTT 409

RESULT 11
US-10-363-483A-40288/c
Sequence 40288, Application US/10363483A
Publication No. US2005006401A1
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
FILE REFERENCE: 82011
CURRENT APPLICATION NUMBER: US/10/363, 483A
CURRENT FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 40712
SEQ ID NO 40288
LENGTH: 619
TYPE: DNA

Query Match 92.7%; Score 20.4; DB 20; Length 619;
Best Local Similarity 95.5%; Pred. No. 30; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTGTGTTTCGTCGGTTT 22
Db 430 TCGTGTGTTTCGTCGGTTT 409

RESULT 12
US-10-363-345A-2025
Sequence 2025, Application US/10363345A
Publication No. US20040234960A1
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Method for determining the degree of methylation of defined
FILE REFERENCE: E01/1227
CURRENT APPLICATION NUMBER: US/10/363, 345A
CURRENT FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 40712
SEQ ID NO 2025
LENGTH: 761
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
OTHER INFORMATION: Cpg-island No: 2025
US-10-363-345A-2025

Query Match 92.7%; Score 20.4; DB 20; Length 761;
Best Local Similarity 95.5%; Pred. No. 31; Mismatches 1; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGTGTGTTTCGTCGGTTT 22
Db 598 TCGTGTGTTTCGTCGGTTT 619

RESULT 13
US-10-363-345A-2026/c
Sequence 2026, Application US/10363345A
Publication No. US20040234960A1
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Method for determining the degree of methylation of defined
TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
FILE REFERENCE: E01/1227
CURRENT APPLICATION NUMBER: US/10/363, 345A
CURRENT FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 40712
SEQ ID NO 2026
LENGTH: 761
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
OTHER INFORMATION: Cpg-island No: 2026
US-10-363-345A-2026

Query Match 92.7%; Score 20.4; DB 20; Length 761;
Best Local Similarity 95.5%; Pred. No. 31; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGTGTGTTTCGTCGGTTT 22
Db 598 TCGTGTGTTTCGTCGGTTT 619

RESULT 14
 US-10-363-483A-2025
 ; Sequence 2025, Application US/10363483A
 ; Publication No. US20050064401A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alexander Olek
 ; APPLICANT: Christian Piepenbrock
 ; TITLE OF INVENTION: diagnosis of illnesses or predisposition to certain
 ; TITLE OF INVENTION: diagnosis of illnesses or predisposition to certain
 ; FILE REFERENCE: 82011
 ; CURRENT APPLICATION NUMBER: US/10/363, 483A
 ; CURRENT FILING DATE: 2003-03-03
 ; NUMBER OF SEQ ID NOS: 40712
 ; SEQ ID NO 2025
 ; LENGTH: 761
 ; TYPE: DNA
 ; FEATURE:
 ; ORGANISM: Artificial Sequence
 ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
 ; OTHER INFORMATION: Cpg-island No: 2025
 ; US-10-363-483A-2025

Query Match 92.7%; Score 20.4; DB 21; Length 761;
 Best Local Similarity 95.5%; Pred. No. 31; Mismatches 0; Indels 0; Gaps 0;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTTCGGCGTTT 22
 Db 598 TCGTCGTTTTCGGCGTTT 619

RESULT 15
 US-10-363-483A-2026/C
 ; Sequence 2026, Application US/10363483A
 ; Publication No. US20050064401A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alexander Olek
 ; APPLICANT: Christian Piepenbrock
 ; APPLICANT: Kurt Berlin
 ; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
 ; TITLE OF INVENTION: diagnosis of illnesses or predisposition to certain
 ; FILE REFERENCE: 82011
 ; CURRENT APPLICATION NUMBER: US/10/363, 483A
 ; CURRENT FILING DATE: 2003-03-03
 ; NUMBER OF SEQ ID NOS: 40712
 ; SEQ ID NO 2026
 ; LENGTH: 761
 ; TYPE: DNA
 ; FEATURE:
 ; ORGANISM: Artificial Sequence
 ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
 ; OTHER INFORMATION: Cpg-island No: 2026
 ; US-10-363-483A-2026

Query Match 92.7%; Score 20.4; DB 21; Length 761;
 Best Local Similarity 95.5%; Pred. No. 31; Mismatches 1; Indels 0; Gaps 0;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTTCGGCGTTT 22
 Db 164 TCGTCGTTTTCGGCGTTT 143

RESULT 16
 US-10-363-345A-7203
 ; Sequence 7203, Application US/10363345A

RESULT 17
 US-10-363-345A-7204/C
 ; Sequence 7204, Application US/10363345A
 ; Publication No. US20040234960A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alexander Olek
 ; APPLICANT: Christian Piepenbrock
 ; APPLICANT: Kurt Berlin
 ; TITLE OF INVENTION: Method for determining the degree of methylation of defined
 ; TITLE OF INVENTION: Method for determining the degree of methylation of defined
 ; FILE REFERENCE: 801/1227
 ; CURRENT APPLICATION NUMBER: US/10/363, 345A
 ; CURRENT FILING DATE: 2003-03-03
 ; NUMBER OF SEQ ID NOS: 40712
 ; SEQ ID NO 7204
 ; LENGTH: 1024
 ; TYPE: DNA
 ; FEATURE:
 ; ORGANISM: Artificial Sequence
 ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
 ; OTHER INFORMATION: Cpg-island No: 7204
 ; US-10-363-345A-7204

Query Match 92.7%; Score 20.4; DB 20; Length 1024;
 Best Local Similarity 95.5%; Pred. No. 32; Mismatches 1; Indels 0; Gaps 0;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTTCGGCGTTT 22
 Db 749 TCGTCGTTTTCGGCGTTT 728

RESULT 18
 US-10-363-483A-7203
 ; Sequence 7203, Application US/10363483A
 ; Publication No. US20050064401A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alexander Olek
 ; APPLICANT: Christian Piepenbrock
 ; APPLICANT: Kurt Berlin
 ; TITLE OF INVENTION: diagnosis of illnesses or predisposition to certain
 ; TITLE OF INVENTION: diagnosis of illnesses or predisposition to certain
 ; FILE REFERENCE: 82011
 ; CURRENT APPLICATION NUMBER: US/10/363, 483A
 ; CURRENT FILING DATE: 2003-03-03
 ; NUMBER OF SEQ ID NOS: 40712

US-10-363-345A-28015

Query Match 88.2%; Score 19.4; DB 21; Length 511;

Best Local Similarity 95.2%; Pred. No. 80; Mismatches 1; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CGTCGTTTCGCGGTIT 22

DB 474 CGTCGTTTCGGCGTTT 494

RESULT 21

US-10-363-345A-28016/c

Query Match 88.2%; Score 19.4; DB 20; Length 511;

Best Local Similarity 95.2%; Pred. No. 80; Mismatches 1; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCGCGTTTCGCGGTIT 22

DB 276 TCGCGTTTCGCGGTIT 297

RESULT 19

US-10-363-483A-7204/c

Query Match 92.7%; Score 20.4; DB 21; Length 1024;

Best Local Similarity 95.5%; Pred. No. 32; Mismatches 1; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCGCGTTTCGCGGTIT 22

DB 276 TCGCGTTTCGCGGTIT 297

GENERAL INFORMATION:

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Kurt Berlin

TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain FILE REFERENCE: 82011 CURRENT APPLICATION NUMBER: US/10/363, 483A CURRENT FILING DATE: 2003-03-03 NUMBER OF SEQ ID NOS: 40712 SEQ ID NO 7204 LENGTH: 1024 TYPE: DNA ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) OTHER INFORMATION: Cpg-island No: 7204

RESULT 20

US-10-363-345A-28015

Query Match 92.7%; Score 20.4; DB 21; Length 1024;

Best Local Similarity 95.5%; Pred. No. 32; Mismatches 1; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCGCGTTTCGCGGTIT 22

DB 749 TCGCGTTTCGCGGTIT 728

GENERAL INFORMATION:

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Kurt Berlin

TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain FILE REFERENCE: 82011 CURRENT APPLICATION NUMBER: US/10/363, 483A CURRENT FILING DATE: 2003-03-03 NUMBER OF SEQ ID NOS: 40712 SEQ ID NO 28015 LENGTH: 1024 TYPE: DNA ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) OTHER INFORMATION: Cpg-island No: 7204

RESULT 21

US-10-363-345A-28016/c

Query Match 88.2%; Score 19.4; DB 20; Length 511;

Best Local Similarity 95.2%; Pred. No. 80; Mismatches 1; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CGTCGTTTCGCGGTIT 22

DB 474 CGTCGTTTCGGCGTTT 494

RESULT 22

US-10-363-483A-28015

Query Match 88.2%; Score 19.4; DB 20; Length 511;

Best Local Similarity 95.2%; Pred. No. 80; Mismatches 1; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CGTCGTTTCGCGGTIT 22

DB 38 CGTCGTTTCGGCGTTT 18

GENERAL INFORMATION:

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Kurt Berlin

TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain FILE REFERENCE: 82011 CURRENT APPLICATION NUMBER: US/10/363, 483A CURRENT FILING DATE: 2003-03-03 NUMBER OF SEQ ID NOS: 40712 SEQ ID NO 28015 LENGTH: 511 TYPE: DNA ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) OTHER INFORMATION: Cpg-island No: 28015

RESULT 23

US-10-363-483A-28015

Query Match 88.2%; Score 19.4; DB 21; Length 511;

Best Local Similarity 95.2%; Pred. No. 80; Mismatches 1; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CGTCGTTTCGCGGTIT 22

DB 474 CGTCGTTTCGGCGTTT 494

RESULT 23
US-10-363-483A-28016/C
; Sequence 28015, Application US/10363483A
; Publication No. US20050064401A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; TITLE OF INVENTION: illnesses
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363, 483A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 28016
; LENGTH: 511
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: Cpg-island No: 28016
; OTHER INFORMATION: Cpg-island No: 28016

Query Match 88.2%; Score 19.4; DB 21; Length 511;
Best Local Similarity 95.2%; Pred. No. 80; Mismatches 1; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mis 1; InDel 0; Gap 0;

Qy 2 CGRCGTTTCGCGCGTTT 22
Db 38 CGTCGTTTCGGGGTTT 18

RESULT 24
US-10-363-45A-35059
; Sequence 35059, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E011227
; CURRENT APPLICATION NUMBER: US/10/363, 345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 35059
; LENGTH: 523
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: Cpg-island No: 35059
; OTHER INFORMATION: Cpg-island No: 35059

Query Match 88.2%; Score 19.4; DB 21; Length 511;
Best Local Similarity 95.2%; Pred. No. 80; Mismatches 1; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mis 1; InDel 0; Gap 0;

Qy 2 CGRCGTTTCGCGCGTTT 22
Db 38 CGTCGTTTCGGGGTTT 18

RESULT 25
US-10-363-345A-35060/C
; Sequence 35060, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; TITLE OF INVENTION: illnesses
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363, 483A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 35060
; LENGTH: 523
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: Cpg-island No: 35060

Query Match 88.2%; Score 19.4; DB 21; Length 523;
Best Local Similarity 95.2%; Pred. No. 80; Mismatches 1; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mis 1; InDel 0; Gap 0;

Qy 2 CGRCGTTTCGCGCGTTT 22
Db 488 CGTCGTTTCGGGGTTT 508

RESULT 26
US-10-363-483A-35059
; Sequence 35059, Application US/10363483A
; Publication No. US20050064401A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; TITLE OF INVENTION: illnesses
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363, 483A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 35059
; LENGTH: 523
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: Cpg-island No: 35059

Query Match 88.2%; Score 19.4; DB 20; Length 523;
Best Local Similarity 95.2%; Pred. No. 80; Mismatches 1; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mis 1; InDel 0; Gap 0;

Qy 2 CGTCGTTTCGCGCGTTT 22
Db 36 OCTCGTTTCGCTCGTTT 16

```

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: Cpg-island No: 35060
US-10-613-483A-35060

Query Match 88.2%; Score 19.4; DB 21; Length 523;
Best Local Similarity 95.2%; Pred. No. 80; Mismatches 1; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 CGTCGTTTTCGGCGTTT 22
Db 36 CGTCGTTTTCGGCGTTT 16

RESULT 28
; Sequence 40325, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; TITLE OF INVENTION: Cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A.
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO: 40325
; LENGTH: 524
; SBQ ID NO: 40325
; LENGTH: 524
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: Cpg-island No: 40325
US-10-363-345A-40325

Query Match 88.2%; Score 19.4; DB 20; Length 524;
Best Local Similarity 95.2%; Pred. No. 80; Mismatches 1; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 CGTCGTTTTCGGCGTTT 22
Db 399 CGTCGTTTTCGGCGTTT 419

RESULT 29
US-10-363-345A-40326/C
; Sequence 40326, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; TITLE OF INVENTION: Cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A.
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SBQ ID NO: 40326
; LENGTH: 524
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: Cpg-island No: 40326
US-10-363-345A-40326

Query Match 88.2%; Score 19.4; DB 20; Length 524;
Best Local Similarity 95.2%; Pred. No. 80; Mismatches 1; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 CGTCGTTTTCGGCGTTT 22
Db 399 CGTCGTTTTCGGCGTTT 419

RESULT 30
US-10-363-483A-40325
; Sequence 40325, Application US/10363483A
; Publication No. US2005064401A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; TITLE OF INVENTION: illnesses
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363,483A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO: 40325
; LENGTH: 524
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: Cpg-island No: 40325
US-10-363-483A-40325

Query Match 88.2%; Score 19.4; DB 21; Length 524;
Best Local Similarity 95.2%; Pred. No. 80; Mismatches 1; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 CGTCGTTTTCGGCGTTT 22
Db 399 CGTCGTTTTCGGCGTTT 419

Search completed: August 29, 2005, 00:03:33
Job time : 376 secs

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Om nucleic - nucleic search, using bw model

Run on: August 28, 2005, 20:09:59 ; Search time 64 Seconds
(w/o alignment)
561.470 Million cell updates/sec

Title: US-10-613-228A-1
Perfect score: 22

Sequence: 1 tcgtcggttttcgtgcgtttt 22

Scoring table: IDENTITY_NTC
Gapop 10⁻, Gapext 1.0

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Searched: 1202784 seqs, 818138359 residues
Post-processing: Minimum Match 0%
Maximum Match 100%

Total number of hits satisfying chosen parameters: 2405568
Listing first 90 summaries

Database : Issued Patents NA:*

1: /cgn2_6/ptodata/1/ina/5A_COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq: *

/cgn2_6/ptodata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB	ID	Description
1	17.2	78.2	133	4	US-09-313-294A-108	Sequence 108, App
2	17.2	78.2	513	4	US-09-107-532A-292	Sequence 292, App
3	16.8	76.4	36016	4	US-09-949-016-14223	Sequence 14223, A
4	16.4	74.5	3531	1	US-08-629-60-0-1	Sequence 1, Appli
5	16.4	74.5	3531	3	US-09-076-761-1	Sequence 1, Appli
6	16.2	73.6	909	4	US-09-134-000-3167	Sequence 3167, AP
7	16.2	73.6	2358	4	US-09-134-000-3285	Sequence 3285, AP
8	15.8	71.8	660	4	US-09-489-039A-560	Sequence 560, APP
9	15.6	70.9	231	4	US-09-541-2772	Sequence 2772, AP
10	15.6	70.9	300	4	US-09-543-681A-1478	Sequence 1478, AP
11	15.6	70.9	440	4	US-09-513-999C-35185	Sequence 35185, A
12	15.6	70.9	599	4	US-09-270-767-3552	Sequence 3552, AP
13	15.6	70.9	599	4	US-09-270-767-18834	Sequence 18834, A
14	15.6	70.9	601	4	US-09-949-016-1352	Sequence 1352, A
15	15.6	70.9	601	4	US-09-949-016-69221	Sequence 69221, A
16	15.6	70.9	601	4	US-09-949-016-81370	Sequence 81370, A
17	15.6	70.9	601	4	US-09-949-016-127420	Sequence 127420, A
18	15.6	70.9	601	4	US-09-949-016-177125	Sequence 177125, A
19	15.6	70.9	601	4	US-09-949-016-177126	Sequence 177126, A
20	15.6	70.9	601	4	US-09-949-016-177127	Sequence 177127, A
21	15.6	70.9	678	3	US-09-134-001C-2551	Sequence 2551, AP
22	15.6	70.9	826	3	US-09-221-017B-1008	Sequence 1008, AP
23	15.6	70.9	850	3	US-08-860B-34	Sequence 34, AP1
24	15.6	70.9	1068	4	US-09-543-681A-2972	Sequence 2972, AP
25	15.6	70.9	1734	4	US-09-248-796A-4704	Sequence 4704, AP
26	15.6	70.9	2109	4	US-09-248-796A-2993	Sequence 2993, AP
27	15.6	70.9	2394	4	US-09-540-236-893	Sequence 893, AP

ALIGNMENTS

Result No.	Score	Query	Match Length	DB	ID	Description
1	17.2	78.2	133	4	US-09-313-294A-108	Sequence 108, App
2	17.2	78.2	513	4	US-09-107-532A-292	Sequence 292, App
3	16.8	76.4	36016	4	US-09-949-016-14223	Sequence 14223, A
4	16.4	74.5	3531	1	US-08-629-60-0-1	Sequence 1, Appli
5	16.4	74.5	3531	3	US-09-076-761-1	Sequence 1, Appli
6	16.2	73.6	909	4	US-09-134-000-3167	Sequence 3167, AP
7	16.2	73.6	2358	4	US-09-134-000-3285	Sequence 3285, AP
8	15.8	71.8	660	4	US-09-489-039A-560	Sequence 560, APP
9	15.6	70.9	231	4	US-09-541-2772	Sequence 2772, AP
10	15.6	70.9	300	4	US-09-543-681A-1478	Sequence 1478, AP
11	15.6	70.9	440	4	US-09-513-999C-35185	Sequence 35185, A
12	15.6	70.9	599	4	US-09-270-767-3552	Sequence 3552, AP
13	15.6	70.9	599	4	US-09-270-767-18834	Sequence 18834, A
14	15.6	70.9	601	4	US-09-949-016-1352	Sequence 1352, A
15	15.6	70.9	601	4	US-09-949-016-69221	Sequence 69221, A
16	15.6	70.9	601	4	US-09-949-016-81370	Sequence 81370, A
17	15.6	70.9	601	4	US-09-949-016-127420	Sequence 127420, A
18	15.6	70.9	601	4	US-09-949-016-177125	Sequence 177125, A
19	15.6	70.9	601	4	US-09-949-016-177126	Sequence 177126, A
20	15.6	70.9	678	3	US-09-134-001C-2551	Sequence 2551, AP
21	15.6	70.9	826	3	US-09-221-017B-1008	Sequence 1008, AP
22	15.6	70.9	850	3	US-08-860B-34	Sequence 34, AP1
23	15.6	70.9	1068	4	US-09-543-681A-2972	Sequence 2972, AP
24	15.6	70.9	1734	4	US-09-248-796A-4704	Sequence 4704, AP
25	15.6	70.9	2109	4	US-09-248-796A-2993	Sequence 2993, AP
26	15.6	70.9	2394	4	US-09-540-236-893	Sequence 893, AP

RESULT 1

US-09-313-294A-108

; Sequence 1008, Application US/09313294A

; GENERAL INFORMATION:

APPLICANT: Lalgudi, Raghunath V.
 APPLICANT: Ito, Laura Y.
 APPLICANT: Sherman, Bradley K.
 TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
 FILE REFERENCE: PL_0017 US
 CURRENT APPLICATION NUMBER: US/09/313,294A
 CURRENT FILING DATE: 1999-05-14
 NUMBER OF SEQ ID NOS: 7600
 SOFTWARE: PERL Program
 SEQ ID NO: 1,08
 LENGTH: 133
 OTHER INFORMATION: a, t, c, g, or other
 ORGANISM: Zea mays
 FEATURE: misc feature
 NAME/KEY: misc feature
 OTHER INFORMATION: Incyte ID No. 6476212 700548545H1
 LOCATION: 8
 LOCATION: (B) LOCATION 1..513
 SEQUENCE DESCRIPTION: SEQ ID NO: 292:
 US-09-107-532A-292
 Query Match 78.2%; Score 17.2; DB 4; Length 133;
 Best Local Similarity 86.4%; Pred. No. 1.2e+02;
 Matches 19; Conservative 0; Mismatches 3;
 QY 1 TCGTGGTTTCGCGGTTT 22
 Db 72 TCGTGGTTTCGCGGTTT 93
 RESULT 2
 US-09-107-532A-292/C
 Sequence 22, Application US/09107532A
 Patent No. 658375
 GENERAL INFORMATION:
 APPLICANT: Lynn A Doucette-Stamm and David Bush
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO
 ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
 NUMBER OF SEQUENCES: 7310
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: THERAPEUTICS CORPORATION
 STREET: 100 Beaver Street
 CITY: Waltham
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02454
 COMPUTER READABLE FORM:
 COMPUTER: PC
 OPERATING SYSTEM: <Unknown>
 SOFTWARE: ASCII
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/107,532A
 FILING DATE: 30-Jun-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/085,598
 FILING DATE: 14 May 1998
 APPLICATION NUMBER: 60/051571
 FILING DATE: July 2, 1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Arinello, Pamela Denke
 REGISTRATION NUMBER: 40 489
 REFERENCE/DOCKET NUMBER: GTC-012
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (781) 893-5007
 TELEFAX: (781) 893-8277
 INFORMATION FOR SEQ ID NO: 292:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 513 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: circular
 MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Enterococcus faecium
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (B) LOCATION 1..513
 SEQUENCE DESCRIPTION: SEQ ID NO: 292:
 US-09-107-532A-292
 Query Match 78.2%; Score 17.2; DB 4; Length 513;
 Best Local Similarity 86.4%; Pred. No. 1.3e+02;
 Matches 19; Conservative 0; Mismatches 3;
 Indels 0; Gaps 0;
 QY 1 TCGTGGTTTCGCGGTTT 22
 Db 76 TCGTGGTTTCGCGGTTT 55
 RESULT 3
 US-09-949-016-14223/C
 Sequence 14223, Application US/09949016
 Patent No. 6812339
 GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CI001307
 CURRENT APPLICATION NUMBER: US/09/949, 016
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 14223
 LENGTH: 36016
 TYPE: DNA
 ORGANISM: Human
 US-09-949-016-14223
 Query Match 76.4%; Score 16.8; DB 4; Length 36016;
 Best Local Similarity 90.0%; Pred. No. 2.7e+02;
 Matches 18; Conservative 0; Mismatches 2;
 Indels 0; Gaps 0;
 QY 3 GRCGTTTCGCGGTTT 22
 Db 31422 GRCGTTTCGCGGTTT 31403
 RESULT 4
 US-08-629-601-1/C
 Sequence 1, Application US/08629600
 Patent No. 578196
 GENERAL INFORMATION:
 APPLICANT: NORIEGA, Fernando
 APPLICANT: LEVINE, Myron M.
 TITLE OF INVENTION: GUA MUTANTS OF SHIGELLA
 TITLE OF INVENTION: AND VACCINES CONTAINING THE SAME
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SUGHRUE, MITCHELL, ZINN, MACPEAK & SEAS
 STREET: 2100 Pennsylvania Avenue, N.W., Suite 800
 CITY: Washington, D.C.
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20037
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/629,600
 FILING DATE: 9-APR-1996
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: KIT, Gordon
 REGISTRATION NUMBER: 30-764
 REFERENCE/DOCKET NUMBER: A-6765
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 293-7060
 TELEFAX: (202) 293-7860
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3531 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: genomic DNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO

US-08-629-600-1

Query Match 74.5%; Score 16.4; DB 1; Length 3531;
 Best Local Similarity 94.4%; Pred. No. 3.3e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 CGTTTTCGTCGGTTT 22
 Db 846 CGTTTTCGTCGGTTT 829

RESULT 5
 US-09-076-761-1/c

Sequence 1, Application US/09076761
 Pat. No. 6190669

GENERAL INFORMATION:
 APPLICANT: NORIEGA, Fernando
 APPLICANT: SZTEIN, Marcelo B.
 APPLICANT: LEVINE, Myron M.
 TITLE OF INVENTION: ATTENUATED MUTANTS OF SALMONELLA
 TITLE OF INVENTION: WHICH CONSTITUTIVELY EXPRESS THE
 TITLE OF INVENTION: VI ANTIGEN
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
 STREET: 2100 Pennsylvania Avenue, N.W., Suite 800
 CITY: Washington, D.C.
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20037

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/076,761
 FILING DATE: 13-MAY-1998
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: KIT, Gordon
 REGISTRATION NUMBER: 30-764
 REFERENCE/DOCKET NUMBER: A-67140
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 293-7060
 TELEFAX: (202) 293-7860
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3531 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single

RESULT 6
 US-09-134-000C-3167/c

Sequence 3167, Application US/09134000C
 Pat. No. 6617156

GENERAL INFORMATION:
 APPLICANT: Lynn Doucette-Stamm et al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
 FILE REFERENCE: 032795-032
 CURRENT APPLICATION NUMBER: US/09/134, 000C
 CURRENT FILING DATE: 1998-08-13
 PRIOR APPLICATION NUMBER: US 60/055, 778
 PRIOR FILING DATE: 1997-08-15
 NUMBER OF SEQ ID NOS: 6812
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 3167
 LENGTH: 909
 TYPE: DNA
 ORGANISM: Enterococcus faecalis

RESULT 7
 US-09-134-000C-3167

Sequence 3285, Application US/09134000C
 Pat. No. 6617156

GENERAL INFORMATION:
 APPLICANT: Lynn Doucette-Stamm et al
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO
 TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 032795-032
 CURRENT APPLICATION NUMBER: US/09/134, 000C
 CURRENT FILING DATE: 1998-08-13
 PRIOR APPLICATION NUMBER: US 60/055, 778
 PRIOR FILING DATE: 1997-08-15
 NUMBER OF SEQ ID NOS: 6812
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 3285
 LENGTH: 2358
 TYPE: DNA
 ORGANISM: Enterococcus faecalis

RESULT 7
 US-09-134-000C-3285

Query Match 73.6%; Score 15.2; DB 4; Length 2358;
 Best Local Similarity 85.7%; Pred. No. 4e+02; Mismatches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 CGTCGTTTCGCGGTWT 22
 Db 1697 CGTCGTTTCGCGGTWT 1677

RESULT 8
US-09-489-039A-560
Sequence 560, Application US/09489039A
Patient No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al.
TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
FILE REFERENCE: 2709.200401
CURRENT APPLICATION NUMBER: US/09/489, 039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 560
LENGTH: 660
TYPE: DNA
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-560

Query Match 71.8%; Score 15.8; DB 4; Length 660;
Best Local Similarity 89.5%; Pred. No. 5.4e+02; Mismatches 17; Conservative 0; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GTCGTTTTCGCGTTT 21
Db 426 GTCGTTTTCGCGATT 444

RESULT 9
US-09-543-681A-2772
Sequence 2772, Application US/09543681A
Patient No. 660509
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543, 681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 2772
LENGTH: 231
TYPE: DNA
ORGANISM: Proteus mirabilis
US-09-543-681A-2772

Query Match 70.9%; Score 15.6; DB 4; Length 300;
Best Local Similarity 81.8%; Pred. No. 6.2e+02; Mismatches 18; Conservative 0; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCGGTTTCGCGTTT 22
Db 167 TCCGGTTTCAGCTTT 188

RESULT 10
US-09-543-681A-1478/C
Sequence 1478, Application US/09543681A
Patient No. 660509
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543, 681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09

Query Match 70.9%; Score 15.6; DB 4; Length 599;
Best Local Similarity 81.8%; Pred. No. 6.5e+02; Mismatches 18; Conservative 0; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCGGTTTCGCGTTT 22
Db 568 TCCGGTTTCGCGTTT 547

RESULT 11
US-09-513-999C-35185
Sequence 35185, Application US/09513999C
Patient No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclos, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513, 999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent-PM
SEQ ID NO 35185
LENGTH: 440
TYPE: DNA
ORGANISM: Homo sapiens
US-09-513-999C-35185

Query Match 70.9%; Score 15.6; DB 4; Length 440;
Best Local Similarity 81.8%; Pred. No. 6.4e+02; Mismatches 18; Conservative 0; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCGGTTTCGCGTTT 22
Db 193 TCCGGTTTCGCGTTT 214

RESULT 12
US-09-270-767-3552/C
Sequence 3552, Application US/09270767
Patient No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et. al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3552
LENGTH: 599
TYPE: DNA
ORGANISM: Drosophila melanogaster
US-09-270-767-3552

Query Match 70.9%; Score 15.6; DB 4; Length 599;
Best Local Similarity 81.8%; Pred. No. 6.5e+02; Mismatches 18; Conservative 0; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCGGTTTCGCGTTT 22
Db 568 TCCGGTTTCGCGTTT 547

RESULT 13
US-09-270-767-18834/C
; Sequence 18834, Application US/09270767
; Patent No. 67033491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
; FILE REFERENCE: File Reference: 7326-194
; CURRENT APPLICATION NUMBER: US/09/270-767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18834
; LENGTH: 599
; TYPE: DNA
; ORGANISM: *Drosophila melanogaster*
US-09-270-767-18834

Query Match	70.9%	Score 15.6;	DB 4;	Length 599;
Best Local Similarity	81.8%	Pred. No. 6.5e+02;	Mismatches 4;	Indels 0;
Matches	18;	Conservative	0;	Gaps 0;
Qy	1 TCGTGTGTTTCGCGGTTT 22			
Db	568 TCGTGTGTTTCGCGGTTT 547			

RESULT 14
US-09-949-016-31352/C
; Sequence 31352, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 31352
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-31352

Query Match	70.9%	Score 15.6;	DB 4;	Length 601;
Best Local Similarity	81.8%	Pred. No. 6.5e+02;	Mismatches 4;	Indels 0;
Matches	18;	Conservative	0;	Gaps 0;
Qy	1 TCGTGTGTTTCGCGGTTT 22			
Db	334 TTGTCCTTTCGGTTT 313			

RESULT 15
US-09-949-016-69221/C
; Sequence 69221, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001007
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 31352
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-69221

Query Match	70.9%	Score 15.6;	DB 4;	Length 601;
Best Local Similarity	81.8%	Pred. No. 6.5e+02;	Mismatches 4;	Indels 0;
Matches	18;	Conservative	0;	Gaps 0;
Qy	1 TCGTGTGTTTCGCGGTTT 22			
Db	334 TTGTCCTTTCGGTTT 313			

RESULT 17
US-09-949-016-127420/C
; Sequence 127420, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498 ;
; PRIOR FILING DATE: 2000-09-08 ;
; NUMBER OF SEQ ID NOS: 207012 ;
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 127420
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-177420
Query Match 70.9%; Score 15.6; DB 4; Length 601;
Best Local Similarity 81.8%; Pred. No. 6.5e+02; Mismatches 4; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Db 330 TCCCTCCTTCTGCTTT 309

RESULT 18
US-09-949-016-177125/c
; Sequence 177125, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 177125
; LENGTH: 601
; ORGANISM: Human
; US-09-949-016-177125
Query Match 70.9%; Score 15.6; DB 4; Length 601;
Best Local Similarity 81.8%; Pred. No. 6.5e+02; Mismatches 4; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Db 146 TCGTCGCATCTCCCTGCGTTT 125

RESULT 19
US-09-949-016-177126/c
; Sequence 177126, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 177126
; LENGTH: 601
; ORGANISM: Human
; US-09-949-016-177126
Query Match 70.9%; Score 15.6; DB 4; Length 601;
Best Local Similarity 81.8%; Pred. No. 6.5e+02; Mismatches 4; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Db 146 TCGTCGCATCTCCCTGCGTTT 125

RESULT 20
US-09-949-016-177127/c
; Sequence 177127, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 177127
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-177127
Query Match 70.9%; Score 15.6; DB 4; Length 601;
Best Local Similarity 81.8%; Pred. No. 6.5e+02; Mismatches 4; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Db 183 TCGTCGCATCTCTGGCTTT 162

RESULT 21
US-09-134-001C-2551/c
; Sequence 2551, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 2551
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
; US-09-134-001C-2551
Query Match 70.9%; Score 15.6; DB 3; Length 678;
Best Local Similarity 81.8%; Pred. No. 6.6e+02; Mismatches 4; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Db 2551 TCGTCGCATCTCTGGCTTT 678

Qy 1 TCGTCGTTTCCTGGTTT 22
 Db 330 TCTTGTCCTCGCATTT 309

RESULT 22
 US-09-221-017B-1008
 Sequence 34, Application US/09221017B
 Patent No. 6133506

GENERAL INFORMATION:
 APPLICANT: Tüper, R., Bautor, J., Bothmann, H., Pilsek, E.,
 APPLICANT: Hvricken-Grandpierre, C., Klein, B., Martini, N.,
 APPLICANT: Müller, A., Schulte, W., Voetz, M., Walek, J.,
 APPLICANT: Schell, J.

TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
 NUMBER OF SEQUENCES: 1120
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FERSTER
 STREET: 755 PAGE MILL ROAD
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304-1018

COMPUTER READABLE FORM:
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows
 SOFTWARE: FastSeq for Windows Version 2.0b

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/221.017B

FILING DATE: 23-DEC-1998
 CLASSIFICATION:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PP1182

FILING DATE: 31-DEC-1997
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: PP1146
 FILING DATE: 30-JAN-1998
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: PP2911
 FILING DATE: 09-APR-1998
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/AU98/01023
 FILING DATE: 10-DEC-1998
 ATTORNEY/AGENT INFORMATION:

NAME: Monroe, Gladys H
 REGISTRATION NUMBER: 32,430
 REFERENCE/DOCKET NUMBER: 277340-20021.00

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-813-5600
 TELEX: 706141
 TELEFAX: 650-494-0792

INFORMATION FOR SEQ ID NO: 1008:
 SEQUENCE CHARACTERISTICS:

LENGTH: 826 base pairs

TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: circular
 MOLECULE TYPE: DNA (genomic)

ANTI-SENSE: UNKNOWN
 ORIGINAL SOURCE:

ORGANISM: Cuphea lanceolata
 IMMEDIATE SOURCE:

LIBRARY: genomic Lambda FIX II
 CLONE: CITE97

FEATURE:
 NAME/KEY: Startcodon
 LOCATION: 783..785

FEATURE:
 NAME/KEY: CDS
 LOCATION: 783..850

US-08-617-860B-34

Query Match 70.9%; Score 15.6; DB 3; Length 826;
 Best Local Similarity 81.8%; Pred. No. 6.7e+02;
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTCCTGGTTT 22
 Db 594 TCTGGTATTTCGAGGAAATT 615

RESULT 23
 US-08-617-860B-34
 Sequence 34, Application US/08617860B
 Patent No. 6133506

GENERAL INFORMATION:
 APPLICANT: Tüper, R., Bautor, J., Bothmann, H., Pilsek, E.,
 APPLICANT: Hvricken-Grandpierre, C., Klein, B., Martini, N.,
 APPLICANT: Müller, A., Schulte, W., Voetz, M., Walek, J.,
 APPLICANT: Schell, J.

TITLE OF INVENTION: Promoters
 NUMBER OF SEQUENCES: 35
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Steinberg, Raskin & Davidson, P.C.
 STREET: 1140 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10036

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS

SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/617,860B

FILING DATE: 01-MAR-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/EP94/02950
 FILING DATE: 05-SEP-1994
 APPLICATION NUMBER: DE 4329951.2
 FILING DATE: 04-SEP-1993
 INFORMATION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:
 LENGTH: 850 Base Pairs
 TYPE: Nucleic acid
 STRANDEDNESS: Double stranded
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Cuphea lanceolata
 IMMEDIATE SOURCE:

LIBRARY: genomic Lambda FIX II
 CLONE: CITE97

FEATURE:
 NAME/KEY: Startcodon
 LOCATION: 783..785

FEATURE:
 NAME/KEY: CDS
 LOCATION: 783..850

US-08-617-860B-34

Query Match 70.9%; Score 15.6; DB 3; Length 850;
 Best Local Similarity 81.8%; Pred. No. 6.7e+02;
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTCCTGGTTT 22
 Db 594 TCTGGTATTTCGAGGAAATT 615

RESULT 24
 US-09-543-681A-2972/C
 Sequence 2272, Application US/09543681A
 Patent No. 6605709

GENERAL INFORMATION:
 APPLICANT: GARY BRETON

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIJ
 FILE REFERENCE: 2709.1002-001

Qy 1 TCGTCGTTTCCTGGTTT 22
 Db 137 TCTTCATTTCTGTCCTTT 158

Query Match 70.9%; Score 15.6; DB 4; Length 2109;
 Best Local Similarity 81.8%; Pred. No. 7.2e+02; Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TCGAGGTTTCTGGGTTT 22
 Db 135 TCCCTGTTTCTAGCTTT 114

RESULT 25
 US-09-48-796A-4704/C
 Sequence 4704, Application US/09248796A
 Patent No. 6747137

GENERAL INFORMATION:
 APPLICANT: Keith Weinstock et al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

FILE REFERENCE: 107196-132
 CURRENT APPLICATION NUMBER: US/09/248,796A
 CURRENT FILING DATE: 1999-02-12
 PRIOR APPLICATION NUMBER: US 60/074,725
 PRIOR FILING DATE: 1998-02-13
 PRIOR FILING DATE: 1998-08-13
 NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 4704
 LENGTH: 1734
 TYPE: DNA

ORGANISM: Candida albicans

US-09-248-796A-4704

Query Match 70.9%; Score 15.6; DB 4; Length 1734;
 Best Local Similarity 81.8%; Pred. No. 7.1e+02; Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TCGCGGTTCCTGGCGTTT 22
 Db 398 TCGTCATTGTTGGCTTT 377

RESULT 26
 US-09-248-796A-2999
 Sequence 2999, Application US/09248796A
 Patent No. 6747137

GENERAL INFORMATION:
 APPLICANT: Keith Weinstock et al
 TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 107196-132
 CURRENT FILING DATE: 1999-02-12
 PRIOR APPLICATION NUMBER: US 60/074,725
 PRIOR FILING DATE: 1998-02-13
 PRIOR FILING DATE: 1998-08-13
 NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 2999
 LENGTH: 2109
 TYPE: DNA

ORGANISM: Candida albicans

US-09-248-796A-2999

Query Match 70.9%; Score 15.6; DB 4; Length 2394;
 Best Local Similarity 81.8%; Pred. No. 7.3e+02; Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TCGCTGTTTCTGGCTTT 22
 Db 1232 TGCCGTTTGGGGCTTT 1211

RESULT 28
 US-09-335-865J-7
 Sequence 7, Application US/08335865J
 Patent No. 6107472

GENERAL INFORMATION:
 APPLICANT: Stackier, Steven A.; Hovens, Christopher M.,
 Wiles, Andrew F.
 TITLE OF INVENTION: RECEPTOR-TYPE TYROSINE KINASE-LIKE MOLECULES
 NUMBER OF SEQUENCES: 21
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fulbright & Jaworski L.L.P.
 STREET: 666 Fifth Ave
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10103
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 720 KB storage
 COMPUTER: IBM PS/2
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: ASCII/Wordperfect

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/335,865J
 FILING DATE: 19-January-1995
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/AU93/00210
 FILING DATE: 10-May-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PL2358
 FILING DATE: 11-May-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Hanson, No. 6107472man D.
 REGISTRATION NUMBER: 30,945
 REFERENCE/DOCKET NUMBER: LUD-5277
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 318-3100

; TELFAX: ; (212) 752-5958
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3069
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-335-865J-7

Query Match 70.9%; Score 15.6; DB 3; Length 3069;
 Best Local Similarity 81.8%; Pred. No. 7.4e+02; Indels 0; Gaps 0;
 Matches 18; Conservative 0; Mismatches 4; DB
 QY 1 TCGTGTGTTTCGTCGGTTT 22
 Db 2938 TTGCTGTTTGTGTTTT 2959

RESULT 29
 US-09-513-729B-10/C
 ; Sequence 10, Application US/09513729B
 ; Patent No. 616591
 ; GENERAL INFORMATION:
 ; APPLICANT: Ian Popoff
 ; APPLICANT: Jacqueline Wyatt
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF B2P TRANSCRIPTION FACTOR 3 EXPRESSION
 ; FILE REFERENCE: RTS-0112
 ; CURRENT APPLICATION NUMBER: US/09/513,729B
 ; CURRENT FILING DATE: 2000-02-24
 ; NUMBER OF SEQ ID NOS: 88
 ; SEQ ID NO 10
 ; LENGTH: 3805
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)...(525)
 ; US-09-513-729B-10

Query Match 70.9%; Score 15.6; DB 3; Length 3805;
 Best Local Similarity 81.8%; Pred. No. 7.5e+02; Indels 0; Gaps 0;
 Matches 18; Conservative 0; Mismatches 4; DB
 QY 1 TCGTGTGTTTCGTCGGTTT 22
 Db 2273 TTGCTGTTTGTGTTTT 2252

Search completed: August 28, 2005, 22:57:21
 Job time : 68 secs

RESULT 30
 US-09-023-655-1443/C
 ; Sequence 143, Application US/09023655
 ; Patent No. 660789
 ; GENERAL INFORMATION:
 ; APPLICANT: Cocks, Benjamin G.
 ; APPLICANT: Susan G. Stuart
 ; APPLICANT: Jeffrey J. Seilhamer
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
 ; TITL OF INVENTION: EXPRESSION
 ; NUMBER OF SEQUENCES: 1508
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 ; STREET: 3174 PORTER DRIVE
 ; CITY: PALO ALTO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94304

COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/023,655

FILING DATE: HEREWITH
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Zeller, Karen J.
 REGISTRATION NUMBER: 37,071
 REFERENCE/DOCKET NUMBER: PA-0001 US
 TELECOMMUNICATION INFORMATION:
 TELPHONE: (650) 845-0555
 TELFAX: (650) 845-4166
 INFORMATION FOR SEQ ID NO: 1443:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3805 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GENBANK
 CLONE: 9559708
 US-09-023-655-1443

Query Match 70.9%; Score 15.6; DB 4; Length 3805;
 Best Local Similarity 81.8%; Pred. No. 7.5e+02; Indels 0; Gaps 0;
 Matches 18; Conservative 0; Mismatches 4; DB
 QY 1 TCGTGTGTTTCGTCGGTTT 22
 Db 2273 TTGCTGTTTGTGTTTT 2252

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